



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 117010

TO: Phillip Gambel
Location: 3e81 / 3c70
Monday, March 22, 2004
Art Unit: 1644
Phone: 272-0844
Serial Number: 09 / 627896

From: Jan Delaval
Location: Biotech-Chem Library
Rem 1A51
Phone: 272-2504

jan.delaval@uspto.gov

Search Notes

SEARCH REQUEST FORM

117010

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 3/22/04
Searcher: aw
Terminal time: _____
Elapsed time: 20 + 15
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site

☒ STIC
☐ CM-1
☐ Pre-S

Type of Search

☒ N.A. Sequence
☒ A.A. Sequence
☐ Structure
☐ Bibliographic

Vendors

☐ IG
☐ STN
☐ Dialog
☐ APS
☐ Geninfo
☐ SDC
☐ DARC/Questel
☒ Other

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2004, 16:12:40 ; Search time 36.9101 Seconds
(without alignments)
947.138 Million cell updates/sec

Title: US-09-627-896B-6
Perfect score: 720
Sequence: 1 MGWNCILFLVTATGVHSQ.....ARAAWMDYWGQTLVTVSS 135

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/PCTUS_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	720	100.0	135	9	US-09-249-011A-6
2	720	100.0	461	9	US-09-249-011A-24
3	627	87.1	135	9	US-09-249-011A-2
4	585.5	81.3	470	14	US-10-216-484-147
5	585.5	81.3	470	14	US-10-384-933-147
6	582.5	80.9	470	14	US-10-216-484-143
7	582.5	80.9	470	14	US-10-384-933-143
8	581.5	80.8	470	14	US-10-216-484-145
9	581.5	80.8	470	14	US-10-384-933-145
10	579.5	80.5	470	14	US-10-216-484-117
11	579.5	80.5	470	14	US-10-384-933-117
12	567.5	78.8	470	14	US-10-216-484-157
13	567.5	78.8	470	14	US-10-384-933-157
14	566.5	78.7	145	14	US-10-216-484-75
15	566.5	78.7	145	14	US-10-384-933-75

16	566.5	78.7	470	14	US-10-216-484-89	Sequence 89, Appl
17	566.5	78.7	470	14	US-10-384-933-89	Sequence 89, Appl
18	563.5	78.3	140	15	US-10-366-709-48	Sequence 48, Appl
19	559.5	77.7	134	14	US-10-160-506-27	Sequence 27, Appl
20	551.5	76.6	140	15	US-10-366-709-50	Sequence 50, Appl
21	547	76.0	515	9	US-09-825-012-38	Sequence 66, Appl
22	547	76.0	517	9	US-09-825-012-68	Sequence 38, Appl
23	547	76.0	519	9	US-09-825-012-76	Sequence 76, Appl
24	547	76.0	519	9	US-09-825-012-80	Sequence 80, Appl
25	547	76.0	521	9	US-09-825-012-71	Sequence 71, Appl
26	547	76.0	525	9	US-09-825-012-85	Sequence 85, Appl
27	547	76.0	527	9	US-09-825-012-43	Sequence 43, Appl
28	547	76.0	529	9	US-09-825-012-95	Sequence 95, Appl
29	547	76.0	531	9	US-09-825-012-90	Sequence 90, Appl
30	547	76.0	729	9	US-09-825-012-52	Sequence 52, Appl
31	547	76.0	730	9	US-09-825-012-49	Sequence 49, Appl
32	547	76.0	731	9	US-09-825-012-46	Sequence 46, Appl
33	547	76.0	739	9	US-09-825-012-61	Sequence 61, Appl
34	547	76.0	740	9	US-09-825-012-58	Sequence 58, Appl
35	547	76.0	741	9	US-09-825-012-55	Sequence 55, Appl
36	545	75.7	135	12	US-10-389-417-32	Sequence 32, Appl
37	545	75.7	135	15	US-10-389-155-32	Sequence 31, Appl
38	530.5	73.7	136	14	US-10-160-232-91	Sequence 91, Appl
39	530.5	73.7	140	14	US-10-283-349-63	Sequence 63, Appl
40	528.5	73.4	464	14	US-10-216-484-9	Sequence 9, Appl
41	528.5	73.4	464	14	US-10-384-933-9	Sequence 9, Appl
42	527	73.2	139	9	US-09-760-723-7	Sequence 7, Appl
43	527	73.2	139	9	US-09-355-925-7	Sequence 125, Appl
44	527	73.2	139	10	US-09-269-921-125	Sequence 7, Appl
45	527	73.2	139	10	US-09-509-098-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1

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US-09-249-011A-6
; Sequence 6, Application US/09249011A
; Patent No. US20020176855A1
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanized
; OTHER INFORMATION: murine anti-human B7-2 heavy chain
US-09-249-011A-6
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Best Local Similarity 100.0%; Pred. No. 2.1e-58;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGWNCIIFLVTATGVHSQVLVQSGAEVKKPGSSVKVSKASGYTFTDYAIQWVRQAP 60
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Db 61 GGQLEWIGVINIYDNTNINQKFKGKATMTVDKSTSTAYMELSSLRSEDYAVYYCARAAW 120
Qy 121 YMDYWGQGLTVTVSS 135
Db 121 YMDYWGQGLTVTVSS 135

RESULT 2

US-09-249-011A-24
; Sequence 24, Application US/09249011A
; Patent No. US20020176855A1
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 24
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-249-011A-24

Query Match 100.0%; Score 720; DB 9; Length 461;
Best Local Similarity 100.0%; Pred. No. 7.9e-58;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MGWNCIIFLVTATGVHSQVLVQSGAEVKKPGSSVKVSKASGYTFTDYAIQWVRQAP 60
Qy 61 GGQLEWIGVINIYDNTNINQKFKGKATMTVDKSTSTAYMELSSLRSEDYAVYYCARAAW 120
Db 61 GGQLEWIGVINIYDNTNINQKFKGKATMTVDKSTSTAYMELSSLRSEDYAVYYCARAAW 120
Qy 121 YMDYWGQGLTVTVSS 135
Db 121 YMDYWGQGLTVTVSS 135

RESULT 3

US-09-249-011A-2
; Sequence 2, Application US/09249011A
; Patent No. US20020176855A1
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTUIDA M.
Query Match 81.3%; Score 585.5; DB 14; Length 470;
Best Local Similarity 81.4%; Pred. No. 1.7e-45;
Matches 114; Conservative 6; Mismatches 15; Indels 5; Gaps 1;
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Db 1 MGWNCIIFLVTATGVHSQVLVQSGAEVKKPGSSVKVSKASGYTFTDYAIQWVRQAP 60
Qy 61 GGQLEWIGVINIYDNTNINQKFKGKATMTVDKSTSTAYMELSSLRSEDYAVYYCARAAW 119
Db 61 GGQLEWIGVINIYDNTNINQKFKGKATMTVDKSTSTAYMELSSLRSEDYAVYYCARAAW 120
Qy 120 ----WYMDYWGQGLTVTVSS 135

; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: Anti-B7-2 heavy chain
US-09-249-011A-2

Query Match 87.1%; Score 627; DB 9; Length 135;
Best Local Similarity 84.4%; Pred. No. 6.8e-50;
Matches 114; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
Qy 1 MGWNCIIFLVTATGVHSQVLVQSGAEVKKPGSSVKVSKASGYTFTDYAIQWVRQAP 60
Db 1 MGWNCIIFLVTATGVHSQVLVQSGAEVKKPGSSVKVSKASGYTFTDYAIQWVRQAP 60
Qy 61 GGQLEWIGVINIYDNTNINQKFKGKATMTVDKSTSTAYMELSSLRSEDYAVYYCARAAW 120
Db 61 AKSLEWIGVINIYDNTNINQKFKGKATMTVDKSSSTAYMELARLTGSDSAIYYCARAAW 120
Qy 121 YMDYWGQGLTVTVSS 135
Db 121 YMDYWGQGLTVTVSS 135

RESULT 4

US-10-216-484-147
; Sequence 147, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CJP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 147
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-147

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 17, 2004, 06:06:31 ; Search time 16.6854 Seconds
(without alignments)
417.701 Million cell updates/sec

Title: US-09-627-896B-6

Perfect score: 720

Sequence: 1 MGNWCIIFLVLTATGVHSG.....ARAAWMDYWGQGLTVTWS 135

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/prodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	545	75.7	135	1	US-07-634-278-19
4	545	75.7	135	1	US-08-477-728-19
5	545	75.7	135	1	US-08-474-040-19
6	545	75.7	135	1	US-08-487-200-19
7	545	75.7	135	2	US-08-303-569B-31
8	545	75.7	135	3	US-08-484-537-19
9	531.5	73.8	163	5	PCT-US91-02942-5
10	530.5	73.7	140	3	US-08-836-561-63
11	530.5	73.7	140	4	US-09-434-122-63
12	530	73.6	467	2	US-07-916-088A-45
13	529.5	73.5	136	5	PCT-US93-11611-11
14	529.5	73.5	138	3	US-08-513-968-44
15	529	73.5	139	2	US-08-656-586-8
16	527	73.2	135	1	US-08-137-117D-102
17	527	73.2	135	4	US-08-436-717-102
18	527	73.2	139	4	US-09-355-925-7
19	526	73.1	133	3	US-08-718-323A-8
20	526	73.1	133	4	US-09-587-526-8
21	525	72.9	139	1	US-08-253-877C-19
22	525	72.9	139	2	US-08-452-164A-19
23	525	72.9	139	3	US-08-603-024-18
24	525	72.9	139	4	US-08-450-809-14
25	523	72.6	139	4	US-09-355-925-8
26	521	72.4	135	1	US-08-137-117D-100
27	521	72.4	135	2	US-08-436-717-100

28 521 72.4 137 3 US-08-513-968-38 Sequence 38, Appl
29 518.5 72.0 140 3 US-08-836-561-74 Sequence 74, Appl
30 518.5 72.0 140 4 US-09-434-122-74 Sequence 74, Appl
31 515.5 71.6 140 3 US-08-836-561-78 Sequence 78, Appl
32 515.5 71.6 140 4 US-09-434-122-78 Sequence 78, Appl
33 515 71.5 135 1 US-08-137-117D-112 Sequence 112, Appl
34 515 71.5 135 2 US-08-436-717-112 Sequence 112, Appl
35 511.5 71.0 136 4 US-08-525-539A-63 Sequence 63, Appl
36 508.5 70.6 143 1 US-08-236-520-7 Sequence 7, Appl
37 508.5 70.6 143 5 PCT-US95-05262-7 Sequence 83, Appl
38 507.5 70.5 140 3 US-08-836-561-83 Sequence 83, Appl
39 507.5 70.5 140 4 US-09-434-122-83 Sequence 43, Appl
40 506 70.3 472 4 US-09-301-593-43 Sequence 8, Appl
41 504.5 70.1 136 4 US-09-450-520A-8 Sequence 28, Appl
42 503.5 69.9 140 1 US-07-946-421-28 Sequence 53, Appl
43 501.5 69.7 123 1 US-08-482-882-53 Sequence 53, Appl
44 501.5 69.7 123 2 US-08-483-389-53 Sequence 53, Appl
45 501.5 69.7 123 2 US-08-487-113D-53 Sequence 53, Appl

ALIGNMENTS

RESULT 1

US-08-579-378A-12
; Sequence 12, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co. Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-579-378A-12		US-07-634-278-19	
Query Match 79.7%; Score 573.5; DB 3; Length 140; Best Local Similarity 78.6%; Pred. No. 5.9e-50; Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;		Query Match 75.7%; Score 545; DB 1; Length 135; Best Local Similarity 77.8%; Pred. No. 3.9e-47; Matches 105; Conservative 7; Mismatches 23; Indels 0; Gaps 0;	
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Db 1 MGWNCILFLVATATGVHSQVLVQSGAEVKKPKGSSVKVSKASGYTFTSYVWHWVRQAP 60	Db 1 MGWNCILFLVATATGVHSQVLVQSGAEVKKPKGSSVKVSKASGYTFTSYVWHWVRQAP 60		
QY 61 GQGLEWIGVINIYDNTNNQKFKGKATMTVDKSTSTAYMELSSLRSEDATVYYCARAAW 120	QY 61 GQGLEWIGVINIYDNTNNQKFKGKATMTVDKSTSTAYMELSSLRSEDATVYYCARAAW 120		
Db 61 GQGLEWIGIYIPYNDGTYKNEKFKGRVTITSDSTNTAYMELSSLRSEDATVYYCAREEY 120	Db 61 GQGLEWIGIYIPYNDGTYKNEKFKGRVTITSDSTNTAYMELSSLRSEDATVYYCAREEY 120		
QY 121 -----YMDYWGQGLTVTVSS 135	QY 121 -----YMDYWGQGLTVTVSS 135		
Db 121 GNVVRYFDVWGQGLTVTVSS 140	Db 121 GNVVRYFDVWGQGLTVTVSS 140		
RESULT 2			
PCT-US93-11612-12			
; Sequence 12, Application PC/TUS9311612			
; GENERAL INFORMATION:			
; APPLICANT: Co. Man Sung			
; TITLE OF INVENTION: Humanized Antibodies Reactive with			
; NUMBER OF SEQUENCES: 12			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Townsend and Townsend Khourie and Crew			
; STREET: One Market Plaza, Steuart Tower, Suite 2000			
; CITY: San Francisco			
; STATE: California			
; COUNTRY: USA			
; ZIP: 94105			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent In Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: PCT/US93/11612			
; FILING DATE:			
; CLASSIFICATION:			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/983,946			
; FILING DATE: 01-DEC-1992			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Smith, William M.			
; REGISTRATION NUMBER: 30,223			
; REFERENCE/DOCKET NUMBER: 11823-22			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 415-326-2400			
; TELEFAX: 415-326-2422			
; INFORMATION FOR SEQ ID NO: 12:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 140 amino acids			
; TYPE: amino acid			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
PCT-US93-11612-12			
Query Match 79.7%; Score 573.5; DB 5; Length 140; Best Local Similarity 78.6%; Pred. No. 5.9e-50; Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;			
QY 1 MGWNCILFLVTTATGVHSQVLVQSGAEVKKPKGSSVKVSKASGYTFTDYAIQWVRQAP 60	QY 1 MGWNCILFLVTTATGVHSQVLVQSGAEVKKPKGSSVKVSKASGYTFTDYAIQWVRQAP 60		
Db 1 MGWNCILFLVATATGVHSQVLVQSGAEVKKPKGSSVKVSKASGYTFTSYVWHWVRQAP 60	Db 1 MGWNCILFLVATATGVHSQVLVQSGAEVKKPKGSSVKVSKASGYTFTSYVWHWVRQAP 60		
QY 61 GQGLEWIGVINIYDNTNNQKFKGKATMTVDKSTSTAYMELSSLRSEDATVYYCARAAW 120	QY 61 GQGLEWIGVINIYDNTNNQKFKGKATMTVDKSTSTAYMELSSLRSEDATVYYCARAAW 120		
Db 61 GQGLEWIGIYIPYNDGTYKNEKFKGRVTITSDSTNTAYMELSSLRSEDATVYYCAREEY 120	Db 61 GQGLEWIGIYIPYNDGTYKNEKFKGRVTITSDSTNTAYMELSSLRSEDATVYYCAREEY 120		

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 18, 2004, 16:12:40 ; Search time 36.0899 seconds

(without alignments)
947.138 Million cell updates/sec

Title: US-09-627-896B-8

Perfect score: 681

Sequence: 1 MDSQAVLILLWVSGTCG.....YCTQSYNLYTFQGTQKVEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/2/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/prodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/prodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	681	100.0	132	9	US-09-249-011A-8
2	677	99.4	239	9	US-09-249-011A-22
3	629	92.4	132	9	US-09-249-011A-4
4	555.5	81.6	240	9	US-09-799-514-8
5	555	81.5	141	14	US-10-390-986-16
6	554.5	81.4	264	15	US-10-264-049-4274
7	553.5	81.3	135	15	US-10-171-452A-1
8	553.5	81.3	135	15	US-10-353-708-1
9	547.5	80.4	240	14	US-10-159-006-36
10	544.5	80.0	134	14	US-10-255-478-58
11	525.5	77.2	133	14	US-10-159-006-24
12	525.5	77.2	240	14	US-10-159-006-28
13	522.5	76.7	174	15	US-10-104-047-3202
14	519.5	76.3	154	9	US-09-925-299-1226
15	519.5	76.3	154	10	US-09-925-299-1226

16	515	75.6	272	14	US-10-207-655-14	Sequence 14, Appl
17	515	75.6	272	14	US-10-053-530-14	Sequence 14, Appl
18	513.5	75.4	495	14	US-10-345-618-4	Sequence 4, Appl
19	505.5	74.2	211	15	US-10-264-049-4266	Sequence 4266, Ap
20	504.5	74.1	113	10	US-09-995-529-6	Sequence 6, Appl
21	504.5	74.1	113	14	US-10-121-464-6	Sequence 6, Appl
22	504.5	74.1	113	14	US-10-159-006-6	Sequence 6, Appl
23	502.5	74.1	113	14	US-10-159-006-34	Sequence 34, Appl
24	502.5	73.8	113	9	US-09-274-163E-16	Sequence 16, Appl
25	502.5	73.8	113	9	US-09-956-206A-80	Sequence 80, Appl
26	502.5	73.8	122	14	US-10-010-729-51	Sequence 51, Appl
27	502.5	73.8	155	14	US-10-345-618-11	Sequence 11, Appl
28	502.5	73.8	267	14	US-10-270-071-36	Sequence 36, Appl
29	502.5	73.8	268	14	US-10-270-071-32	Sequence 32, Appl
30	502.5	73.8	268	14	US-10-328-190-2	Sequence 2, Appl
31	502.5	73.8	268	14	US-10-328-190-4	Sequence 4, Appl
32	502.5	73.8	342	14	US-10-345-618-6	Sequence 6, Appl
33	500.5	73.5	113	14	US-10-121-464-2	Sequence 2, Appl
34	500.5	73.5	113	14	US-10-159-006-2	Sequence 2, Appl
35	500.5	73.5	113	14	US-10-159-006-32	Sequence 32, Appl
36	500.5	73.5	432	12	US-10-389-223A-10	Sequence 10, Appl
37	500.5	73.5	480	12	US-10-389-223A-4	Sequence 4, Appl
38	500.5	73.5	614	12	US-10-389-223A-2	Sequence 2, Appl
39	498.5	73.2	114	9	US-09-274-163E-2	Sequence 2, Appl
40	498.5	73.2	114	9	US-09-274-163E-6	Sequence 6, Appl
41	498.5	73.2	274	14	US-10-255-478-66	Sequence 66, Appl
42	498	73.1	113	14	US-10-270-071-8	Sequence 8, Appl
43	497.5	73.1	114	9	US-09-274-163E-4	Sequence 4, Appl
44	497.5	73.1	114	14	US-10-125-687-11	Sequence 11, Appl
45	493.5	72.5	119	14	US-10-010-729-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1

US-09-249-011A-8
Sequence 8, Application US/09249011A

Patent No. US20020176855A1

GENERAL INFORMATION:

APPLICANT: CO. MAN SUNG

APPLICANT: VASQUEZ, MAXIMILIANO

APPLICANT: CARRENO, BEATRIZ

APPLICANT: CELNIKER, ABBIE CHERYL

APPLICANT: COLLINS, MARY

APPLICANT: GOLDMAN, SAMUEL

APPLICANT: GRAY, GARY S.

APPLICANT: KNIGHT, ANDREA

APPLICANT: O'HARA, DENISE

APPLICANT: RUF, BONITA

APPLICANT: VELDMAN, GEERTRUIDA M.

TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS

TITLE OF INVENTION: OF TREATMENT THEREWITH

FILE REFERENCE: 08702.0081-00000

CURRENT APPLICATION NUMBER: US/09/249,011A

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 8

LENGTH: 132

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Humanized

OTHER INFORMATION: murine anti-human B7-2 light chain

US-09-249-011A-8

Query Match 100.0%; Score 681; DB 9; Length 132;

Best Local Similarity 100.0%; Pred. No. 1.3e-53;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MDSQAVLILLWVSGTCGDIVLTQSPDLSIYGLGERATISCKSSGLNSRTRENYLA 60

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Db 1 MDSQAQVLLILLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLA 60
QY 61 WYQKQGPQPKLLIYWASTRESGVDPDRFSGSGSGTDTLTITSSLOAEDVAVYYCTQSYNL 120
Db 61 WYQKQGPQPKLLIYWASTRESGVDPDRFSGSGSGTDTLTITSSLOAEDVAVYYCTQSYNL 120
QY 121 YTFGGQTKVEIK 132
Db 121 YTFGGQTKVEIK 132

RESULT 2

US-09-249-011A-22
; Sequence 22, Application US/09249011A
; Patent No. US20020176855A1
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-249-011A-22

Query Match 99.4%; Score 677; DB 9; Length 239;
Best Local Similarity 99.2%; Pred. No. 5,6e-53;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDSQAQVLLILLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLA 60
Db 1 MDSQAQVLLILLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLA 60
QY 61 WYQKQGPQPKLLIYWASTRESGVDPDRFSGSGSGTDTLTITSSLOAEDVAVYYCTQSYNL 120
Db 61 WYQKQGPQPKLLIYWASTRESGVDPDRFSGSGSGTDTLTITSSLOAEDVAVYYCTQSYNL 120
QY 121 YTFGGQTKVEIK 132
Db 121 YTFGGQTKVEIK 132

RESULT 3

US-09-249-011A-4
; Sequence 4, Application US/09249011A
; Patent No. US20020176855A1
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTUIDA M.

; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: Anti-B7-2 light chain
US-09-249-011A-4

Query Match 92.4%; Score 629; DB 9; Length 132;
Best Local Similarity 90.9%; Pred. No. 6e-49;
Matches 120; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
QY 1 MDSQAQVLLILLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLA 60
Db 1 MDSQAQVLLILLWVSGTCGDIVLTQSPDSLAVSAGEKVTMTCKSSQSLNSRTRENYLA 60
QY 61 WYQKQGPQPKLLIYWASTRESGVDPDRFSGSGSGTDTLTITSSLOAEDVAVYYCTQSYNL 120
Db 61 WYQKQGPQPKLLIYWASTRESGVDPDRFSGSGSGTDTLTITSSLOAEDVAVYYCTQSYNL 120
QY 121 YTFGGQTKVEIK 132
Db 121 YTFGGQTKVEIK 132

RESULT 4

US-09-799-514-8
; Sequence 8, Application US/09799514
; Patent No. US20020065220A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and
; FILE REFERENCE: PT015PI
; CURRENT APPLICATION NUMBER: US/09/799,514
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT/US00/23662
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 60/152,248
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-514-8

Query Match 81.6%; Score 555.5; DB 9; Length 240;
Best Local Similarity 83.1%; Pred. No. 4.5e-42;
Matches 108; Conservative 9; Mismatches 12; Indels 1; Gaps 1;
QY 4 QAQVLLILLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLA 63
Db 4 QTQVFISSLWISGAYGDIWMTQSPDSLAVSLGERATINCKSSQTVLYSSDNKNYLA 63
QY 64 QKQGPQPKLLIYWASTRESGVDPDRFSGSGSGTDTLTITSSLOAEDVAVYYCTQSYNL-YT 122
Db 64 QKQGPQPKLLIYWASTRESGVDPDRFSGSGSGTDTLTITSSLOAEDVAVYYCTQSYNPYS 123
QY 123 FGQGTKEIK 132
Db 124 FGQGTKEIK 133

RESULT 5

US-10-390-986-16

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 17, 2004, 06:06:31 ; Search time 16.3146 Seconds
(without alignments)
417.701 Million cell updates/sec

Title: US-09-627-896B-8
Perfect score: 681
Sequence: 1 MDSQAQVLLILLWVSGTGC.....YCTQSYNLYTFQGQTKVEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	592	86.9	239	1	US-08-353-400-37
2	555	81.5	141	4	US-09-582-337-16
3	553.5	81.3	135	3	US-08-812-586-46
4	553.5	81.3	135	4	US-09-535-832A-43
5	548.5	80.5	133	3	US-08-463-903-4
6	548.5	80.5	133	4	US-07-935-695-4
7	548	80.5	241	2	US-07-916-098A-56
8	547.5	80.4	240	4	US-09-301-593-36
9	544.5	80.0	134	4	US-08-961-309-58
10	528.5	77.6	133	2	US-08-822-028-12
11	528.5	77.6	133	3	US-08-479-285-12
12	528.5	77.6	133	4	US-09-503-613A-12
13	526.5	77.3	133	5	PCT-US93-11611-2
14	525.5	77.2	133	4	US-09-301-593-24
15	525.5	77.2	240	4	US-08-301-593-28
16	522.5	76.7	154	3	US-08-513-968-36
17	513.5	75.4	495	3	US-08-828-741B-4
18	513.5	75.4	495	4	US-09-160-567-4
19	513.5	75.4	495	4	US-09-710-299-4
20	513.5	75.4	495	4	US-09-509-031-4
21	512.5	75.3	133	3	US-08-579-378A-2
22	512.5	75.3	133	5	PCT-US93-11612-2
23	504.5	74.1	113	4	US-09-301-593-6
24	504.5	74.1	113	4	US-09-301-593-34
25	502.5	73.8	113	4	US-08-525-539A-80
26	502.5	73.8	113	4	US-09-274-163E-16
27	502.5	73.8	155	3	US-08-828-741B-11

28	502.5	73.8	155	4	US-09-160-567-11	Sequence 11, Appl
29	502.5	73.8	155	4	US-09-710-299-11	Sequence 11, Appl
30	502.5	73.8	155	4	US-09-509-031-11	Sequence 11, Appl
31	502.5	73.8	342	3	US-08-828-741B-6	Sequence 6, Appl
32	502.5	73.8	342	4	US-09-160-567-6	Sequence 6, Appl
33	502.5	73.8	342	4	US-09-710-299-6	Sequence 6, Appl
34	502.5	73.8	342	4	US-09-509-031-6	Sequence 6, Appl
35	500.5	73.5	113	4	US-09-301-593-2	Sequence 2, Appl
36	500.5	73.5	113	4	US-09-301-593-32	Sequence 32, Appl
37	500.5	73.5	114	4	US-09-025-769B-17	Sequence 17, Appl
38	498.5	73.2	113	5	PCT-US93-08435-8	Sequence 8, Appl
39	498.5	73.2	114	4	US-09-274-163E-2	Sequence 2, Appl
40	498.5	73.2	114	4	US-09-274-163E-6	Sequence 6, Appl
41	498.5	73.2	274	4	US-08-961-309-66	Sequence 66, Appl
42	498.5	73.2	275	3	US-08-463-903-6	Sequence 6, Appl
43	498.5	73.2	275	4	US-07-935-695-6	Sequence 6, Appl
44	497.5	73.1	114	4	US-09-274-163E-4	Sequence 4, Appl
45	497.5	73.1	115	4	US-09-025-769B-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-08-353-400-37
; Sequence 37, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-353-400-37

Query Match 86.9%; Score 592; DB 1; Length 239;
Best Local Similarity 84.8%; Pred. No. 7.8e-48;
Matches 112; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY	1	MDSQAQVLLILLWVSGTGDIVLTQSPDSLAVSLGERATISCKSQSLNSRTRNYLA	60
DB	1	MDSQAQVLLILLWVSGTGDIVMSQSPSLAVSAGEKVTMSCKSQSLNSRTRKNYLA	60
QY	61	WYQKQGPQPKLIYWAISTRESGVPRFSGSGGTDTLTITISIQADVAVYCTQSYNL	120
DB	61	WYQRPQSPKLIYWAISTRTSGVPRFTGSGGTDTLTITISVQAEADLAIYCKQSYTL	120
QY	121	YTFGQGTKEIK	132
DB	121	RTFGGQTKLEIK	132

RESULT 2

US-09-582-337-16
; Sequence 16, Application US/09582337
; Patent No. 6562618
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; FILE REFERENCE: JI-009PCT
; CURRENT APPLICATION NUMBER: US/09/582,337
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-582-337-16

Query Match 81.5%; Score 555; DB 4; Length 141;
Best Local Similarity 82.4%; Pred. No. 1.2e-44;
Matches 108; Conservative 9; Mismatches 12; Indels 2; Gaps 1;

Qy 4 QAOVLILLVWVGTCGDIVLTQSPDSLAVSLGERATISCKSSOSLNSRTRENYLAWYQ 63
Db 4 QTQVFISLLWISGAYGDIWMTQSPDSLAVSLGERATINCKSSQSLIYSSNNKNYLAWYQ 63

Qy 64 QKPGQPPKLLIYWASTRESGVDPDRFSGSGGTFTLTISQLQADVDVAVYCTQSYNL--Y 121
Db 64 QKPGQPPKLLIYWASTRESGVDPDRFSGSGGTFTLTISQLQADVDVAVYCTQSYNL--Y 121

Qy 122 TFGQGTKVEIK 132
Db 124 TFGQGTKVEIK 134

RESULT 3
US-08-812-586-46
; Sequence 46, Application US/08812586
; Patent No. 6048704
; GENERAL INFORMATION:
; APPLICANT: Martin David Tilson
; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)
; TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,586
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/53862-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-812-586-46

Query Match 81.3%; Score 553.5; DB 3; Length 135;
Best Local Similarity 84.6%; Pred. No. 1.6e-44;
Matches 110; Conservative 5; Mismatches 14; Indels 1; Gaps 1;

Qy 4 QAOVLILLVWVGTCGDIVLTQSPDSLAVSLGERATISCKSSOSLNSRTRENYLAWYQ 63
Db 4 QTQVFISLLWISGAYGDIWMTQSPDSLAVSLGERATINCKSSQSLIYSSNNKNYLAWYQ 63

Qy 64 QKPGQPPKLLIYWASTRESGVDPDRFSGSGGTFTLTISQLQADVDVAVYCTQSYNL-YT 122
Db 64 QKPGQPPKLLIYWASTRESGVDPDRFSGSGGTFTLTISQLQADVDVAVYCTQSYNL-YT 122

Qy 123 FGOGTKVEIK 132
Db 124 FGOGTKVEIK 133

RESULT 4
US-09-535-832A-43
; Sequence 43, Application US/09535832A
; Patent No. 6537769
; GENERAL INFORMATION:
; APPLICANT: Tilson, Martin David
; TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated
; TITLE OF INVENTION: with Abdominal Aortic Aneurysm (AAA) Disease, and
; TITLE OF INVENTION: Diagnostic and Therapeutic use Thereof
; FILE REFERENCE: 53862-AZ
; CURRENT APPLICATION NUMBER: US/09/535,832A
; CURRENT FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-832A-43

Query Match 81.3%; Score 553.5; DB 4; Length 135;
Best Local Similarity 84.6%; Pred. No. 1.6e-44;
Matches 110; Conservative 5; Mismatches 14; Indels 1; Gaps 1;

Qy 4 QAOVLILLVWVGTCGDIVLTQSPDSLAVSLGERATISCKSSOSLNSRTRENYLAWYQ 63
Db 4 QTQVFISLLWISGAYGDIWMTQSPDSLAVSLGERATINCKSSQSLIYSSNNKNYLAWYQ 63

Qy 64 QKPGQPPKLLIYWASTRESGVDPDRFSGSGGTFTLTISQLQADVDVAVYCTQSYNL-YT 122
Db 64 QKPGQPPKLLIYWASTRESGVDPDRFSGSGGTFTLTISQLQADVDVAVYCTQSYNL-YT 122

Qy 123 FGOGTKVEIK 132
Db 124 FGOGTKVEIK 133

RESULT 5
US-08-463-903-4
; Sequence 4, Application US/08463903
; Patent No. 6071515
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S.
; APPLICANT: Richard, Ruth A.
; APPLICANT: Affholter, Joseph A.
; APPLICANT: Kotite, Nicolas J.
; TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
; FILE REFERENCE: 40224A US

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 08:34:11 ; Search time 555.701 Seconds
(without alignments)

13047.203 Million cell updates/sec

Title: US-09-627-896b-21

Perfect score: 1960

Sequence: 1 tctagaccaccatgattca.....ccactttagatcaattc 1960

Scoring table: IDENTITY_NUC

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Searched: 2438257 seqs, 1849576744 residues

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA.*

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18: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1044	53.3	3881	13	US-10-000-433-1
5	776.4	39.6	1721	15	US-10-291-265-96
6	776.4	39.6	1736	15	US-10-291-265-98
7	776.4	39.6	1741	15	US-10-291-265-97
8	698	35.6	8068	14	US-10-159-006-27
9	694.2	35.4	1710	15	US-10-291-265-99
10	667.6	34.1	8068	14	US-10-159-006-35
11	595.8	30.4	1244	9	US-09-954-456-771
12	595.8	30.4	1244	10	US-09-960-706-696
13	595.8	30.4	1244	10	US-09-873-319-438
14	523.4	26.7	948	9	US-09-859-053-33
15	523.4	26.7	1045	14	US-10-198-846-13629

16	523	26.7	941	9	US-09-800-729-81
17	523	26.7	968	10	US-09-992-600A-7
18	523	26.7	968	10	US-09-924-340-7
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20	523	26.7	968	10	US-09-999-570-7
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23	523	26.7	968	14	US-10-154-678-7
24	523	26.7	968	14	US-10-001-142-7
25	522.8	26.7	913	9	US-09-822-830A-531
26	522.4	26.7	1404	15	US-10-291-265-663
27	522	26.6	1810	15	US-10-108-260A-1650
28	518.4	26.4	970	9	US-09-859-053-37
29	518.4	26.4	974	9	US-09-859-053-29
30	518.4	26.4	990	9	US-09-800-729-79
31	518.4	26.4	1033	9	US-09-799-514-2
32	518.4	26.4	1106	15	US-10-264-049-121
33	518.4	26.4	1230	14	US-10-158-646-59
34	518.4	26.4	1450	15	US-10-291-265-568
35	518.4	26.4	1450	15	US-10-291-265-569
36	518.4	26.4	1450	15	US-10-291-265-570
37	518.4	26.4	1450	15	US-10-291-265-571
38	518.2	26.4	929	15	US-10-108-260A-1838
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44	506.4	25.8	1202	14	US-10-158-646-57
45	504.8	25.8	928	14	US-10-221-945-5

ALIGNMENTS

RESULT 1

US-09-249-011A-21
; Sequence 21, Application US/09249011A
; Patent No. US20020176855A1

GENERAL INFORMATION:

; APPLICANT: CO. MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELMIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 1960
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (12)..(408)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (768)..(1087)
; US-09-249-011A-21

Query Match 100.0%; Score 1960; DB 9; Length 1960;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1960; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTAGACCAACCAATGGAATTCACAGGCCACAGGTTCTTATATATGCTGCTATGGGTATCTG 60
Db 1 TCTAGACCAACCAATGGAATTCACAGGCCACAGGTTCTTATATATGCTGCTATGGGTATCTG 60
QY 61 GCACCTGTGGGACATTTGCTGACACAGTCTCCAGATTCCTGGCTGTAAGCTTAGGAG 120
Db 61 GCACCTGTGGGACATTTGCTGACACAGTCTCCAGATTCCTGGCTGTAAGCTTAGGAG 120
QY 121 AGAGGGCCACTATTAGCTGCAAAATCCAGTCCAGTCTGCTCAACAGTAGAACCCGAGAGA 180
Db 121 AGAGGGCCACTATTAGCTGCAAAATCCAGTCCAGTCTGCTCAACAGTAGAACCCGAGAGA 180
QY 181 ACTACTTGCTTGGTACAGACAGAAACCCAGGCGAGCTCTTAACCTGCTGATCTACTGGG 240
Db 181 ACTACTTGCTTGGTACAGACAGAAACCCAGGCGAGCTCTTAACCTGCTGATCTACTGGG 240
QY 241 CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTT 300
Db 241 CATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTT 300
QY 301 TCACCTCTCACCAATCAGCAGTCTCAGGCTGAAGACGTGGCAGTTTATTAATCTGAGCCAAAT 360
Db 301 TCACCTCTCACCAATCAGCAGTCTCAGGCTGAAGACGTGGCAGTTTATTAATCTGAGCCAAAT 360
QY 361 CTTATTAATCTTTACAGTTTCGGACAGGGGACCAAGTGGGAATAAAGCTGAAGTACTCTT 420
Db 361 CTTATTAATCTTTACAGTTTCGGACAGGGGACCAAGTGGGAATAAAGCTGAAGTACTCTT 420
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Db 421 CTCAACTCTAGAAATCTAAACTCTGAGGGGGTCCGATGACGTGGCCATTTCTTTGGCTAA 480
QY 481 AGCATTGAGTTTACTGCAAGGTGAGAAAGCATGCAAGCCCTCAGATGGCTGCAAGA 540
Db 481 AGCATTGAGTTTACTGCAAGGTGAGAAAGCATGCAAGCCCTCAGATGGCTGCAAGA 540
QY 541 GCTCCCAACAAACAAATTTAGAACTTTTATTAAGGAATAGGGGAGCTAGGAAGAACTCA 600
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QY 601 AAACATCAAGATTTTAAATACGCTTCTTGCTCTCTTCTGCTATATTAATCTGGGATAAGCA 660
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QY 1201 ATCTTTCACTCACCCTCCTCCTCCTGCTGCTTGAATTAATATGCTAAATCTGGAGAGAA 1260
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Db 1261 TGAATAAATAAAGTGAATCTTTGCACTGTGTGCTCTCTCTTCTCTCTTCAATTAATAT 1320
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Db 1321 TATCTGTTGTTTACCACTACTCAATTTCTCTTATAGGGACTAATAATAGTAGTCATCC 1380
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Db 1381 TAAGCGCATACCACTTTTATAAAATCATCCTTCTTCTTATTTTACCTTATCATCTCTG 1440
QY 1441 CAAGACAGTCTCTCCTCAAACCCCAAGCCTTCTGTCTCACAAGTCCCTGGGCGATGGT 1500
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QY 1501 AGGAGAGACTGCTGCTGCTTGTCTTCTTCTCCTCAGCAAGCCCTCATAGTCTTTTAAAG 1560
Db 1501 AGGAGAGACTGCTGCTGCTTGTCTTCTTCTCCTCAGCAAGCCCTCATAGTCTTTTAAAG 1560
QY 1561 GTGACAGTCTTACAGTCAATATCTTGTGATTCATTTCCCTGGGAATCAACCAAGCAA 1620
Db 1561 GTGACAGTCTTACAGTCAATATCTTGTGATTCATTTCCCTGGGAATCAACCAAGCAA 1620
QY 1621 ATTTTCAAAGAGAAACCTGCTATAAGAGAAATCATTCATTGCAACATGATATAAAT 1680
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QY 1681 AACACACAAATAAAGCAATTAATAAACAATAAGAGAAATGTTTAAAGTTCATCATG 1740
Db 1681 AACACACAAATAAAGCAATTAATAAACAATAAGAGAAATGTTTAAAGTTCATCATG 1740
QY 1741 GTACTTAGACTTAATGGAATGTCATGCCITATTTTAAACAGGTACTGAGGAC 1800
Db 1741 GTACTTAGACTTAATGGAATGTCATGCCITATTTTAAACAGGTACTGAGGAC 1800
QY 1801 TCCTGCTGCAAGGGCCGTTTGGATCTTTTCCACAACCTTAATCCACACTATAC 1860
Db 1801 TCCTGCTGCAAGGGCCGTTTGGATCTTTTCCACAACCTTAATCCACACTATAC 1860
QY 1861 TGTGAGATTAATAACATTCATTAATGTTGCAAGGTTCTATAAGCTGAGACAAAT 1920
Db 1861 TGTGAGATTAATAACATTCATTAATGTTGCAAGGTTCTATAAGCTGAGACAAAT 1920
QY 1921 ATATTCTATAACTCAGCAATCCCACTTCTAGGATCAATTC 1960
Db 1921 ATATTCTATAACTCAGCAATCCCACTTCTAGGATCAATTC 1960

RESULT 2

US-10-138-727A-40
; Sequence 40, Application US/10138727A
; Publication No. US20030157054A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Susan
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/10/138,727A
; CURRENT FILING DATE: 2002-05-03

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Run on: March 20, 2004, 08:34:11 ; Search time 637.638 Seconds
(without alignments)
13047.203 Million cell updates/sec

Title: US-09-627-896B-23

Perfect score: 2249

Sequence: 1 tctgaccacacacgggttg.....ccgggtaaatgagtgatc 2249

Scoring table: IDENTITY NUC

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Searched: 2438257 seqs, 1849576744 residues

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Published Applications NA:*

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- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1745	77.6	10494	14	Sequence 55, Appl
4	1638	72.8	4694	13	Sequence 40, Appl
5	1613	71.7	2028	13	Sequence 57, Appl
6	1611.8	71.7	4723	13	Sequence 2, Appl
7	1586.2	70.5	11228	15	Sequence 6, Appl
8	1584.6	70.5	2482	8	Sequence 4, Appl
9	1584.6	70.5	2482	9	Sequence 3, Appl
10	1580.4	70.3	1999	14	Sequence 29, Appl
11	1548	68.8	2770	13	Sequence 2, Appl
12	1547.2	68.8	2009	12	Sequence 4, Appl
13	1547.2	68.8	2009	13	Sequence 54, Appl
14	1463.4	65.1	2071	14	Sequence 116, App
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27	1441.2	64.1	2002	14	US-10-401-344-1
28	1438.6	64.0	3282	14	US-10-016-986-154
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31	1438.6	64.0	13254	14	US-10-016-986-156
32	1438.6	64.0	13254	14	US-10-016-986-170
33	1432.4	63.7	7561	12	US-10-395-894-7
34	1431.8	63.7	7558	12	US-10-395-894-5
35	1431.8	63.7	7570	12	US-10-395-894-2
36	1431.8	63.7	7576	12	US-10-395-894-4
37	1431.8	63.7	7579	12	US-10-395-894-3
38	1431.8	63.7	7597	12	US-10-397-569-5
39	1431.8	63.7	9291	15	US-10-267-286A-1
40	1426.4	63.4	2399	14	US-10-185-318-1
41	1093.8	48.6	11265	14	US-10-185-799-1
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43	1092.8	48.6	1459	14	US-09-822-851B-4
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ALIGNMENTS

RESULT 1

US-09-249-011A-23
; Sequence 23, Application US/09249011A
; Patent No. US20020176855A1
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELMIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 2249
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (12)..(417)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (655)..(948)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1341)..(1376)
; NAME/KEY: CDS


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; LOCATION: (1495) .. (1821)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1919) .. (2238)
US-09-249-011A-23

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Query Match 100.0%; Score 2249; DB 9; Length 2249;

[illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 08:27:41 ; Search time 130.901 Seconds
(without alignments)
9534.601 Million cell updates/sec

Title: US-09-627-896B-23
Perfect score: 2249
Sequence: 1 tctagaccacatgggttgg.....ccgggtaaatgagtgatc 2249

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1804	80.2	2560	2	Sequence 44, Appl
2	1742.6	77.5	2287	5	Sequence 8, Appl
3	1651.6	73.4	2287	1	Sequence 1, Appl
4	1651.6	73.4	2287	1	Sequence 1, Appl
5	1651.6	73.4	2287	2	Sequence 1, Appl
6	1651.6	73.4	2287	4	Sequence 1, Appl
7	1611.8	71.7	4723	3	Sequence 370, Appl
8	1611.8	71.7	4723	4	Sequence 218, Appl
9	1610.8	71.6	2029	2	Sequence 43, Appl
10	1584.6	70.5	2482	3	Sequence 3, Appl
11	1584.6	70.5	2482	3	Sequence 3, Appl
12	1584.6	70.5	2482	3	Sequence 3, Appl
13	1584.6	70.5	2482	4	Sequence 3, Appl
14	1584.6	70.5	2482	4	Sequence 3, Appl
15	1584.6	70.5	2482	5	Sequence 3, Appl
16	1584.6	70.5	2482	5	Sequence 3, Appl
17	1580.4	70.3	1999	4	Sequence 54, Appl
18	1548	68.8	2770	4	Sequence 29, Appl
19	1545.6	68.7	2009	1	Sequence 5, Appl
20	1516.2	67.4	1980	1	Sequence 4, Appl
21	1487.4	66.1	10785	3	Sequence 27, Appl
22	1487.4	66.1	10785	4	Sequence 27, Appl
23	1438.6	64.0	3282	1	Sequence 154, Appl
24	1438.6	64.0	3282	1	Sequence 169, Appl
25	1438.6	64.0	3282	1	Sequence 154, Appl
26	1438.6	64.0	3282	1	Sequence 169, Appl
27	1438.6	64.0	3282	1	Sequence 154, Appl

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c 30 1438.6 64.0 3282 5 PCT-US95-08743-169 Sequence 169, App
c 31 1438.6 64.0 3254 1 US-08-276-852-156 Sequence 156, App
c 32 1438.6 64.0 3254 1 US-08-276-852-170 Sequence 170, App
c 33 1438.6 64.0 3254 1 US-08-899-575-156 Sequence 156, App
c 34 1438.6 64.0 3254 1 US-08-899-575-170 Sequence 170, App
c 35 1438.6 64.0 3254 1 US-08-899-575-156 Sequence 156, App
c 36 1438.6 64.0 3254 1 US-08-899-575-170 Sequence 170, App
c 37 1438.6 64.0 3254 5 PCT-US95-08743-156 Sequence 156, App
c 38 1438.6 64.0 3254 5 PCT-US95-08743-170 Sequence 170, App
c 39 1437 63.9 4926 3 US-09-042-353-418 Sequence 418, App
c 40 1437 63.9 4926 4 US-08-758-417A-268 Sequence 268, App
c 41 1435.8 63.8 8614 4 US-09-247-352-5 Sequence 5, Appl
c 42 1435.8 63.8 8614 4 US-09-466-635-5 Sequence 5, Appl
c 43 1426.4 63.4 2399 2 US-08-070-116A-1 Sequence 1, Appl
c 44 1426.4 63.4 2399 4 US-08-557-050-1 Sequence 1, Appl
c 45 1410.4 62.7 10844 3 US-08-444-644-41 Sequence 41, Appl

ALIGNMENTS

RESULT 1

US-07-916-098A-44

; Sequence 44, Application US/07916098A

; Patent No. 5871732

; GENERAL INFORMATION:

; APPLICANT: BURKLY, LINDA C.

; APPLICANT: CHISHOLM, PATRICIA L.

; APPLICANT: THOMAS, DAVID W.

; APPLICANT: ROSA, MARGARET D.

; APPLICANT: ROSA, JOSEPH J.

; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN

; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION

; NUMBER OF SEQUENCES: 61

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.

; STREET: 10 SOUTH WACKER DRIVE

; CITY: CHICAGO

; STATE: ILLINOIS

; COUNTRY: U.S.A.

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/916,098A

; FILING DATE: July 24, 1992

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US91/08843

; FILING DATE: No. 5871732ember 27, 1991

; CLASSIFICATION: 424

; APPLICATION NUMBER: 07/618,542

; FILING DATE: No. 5871732ember 27, 1990

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: JOHN J. MC DONNELL

; REGISTRATION NUMBER: 26,949

; REFERENCE/DOCKET NUMBER: 92,310-G

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 715-1000

; TELEFAX: (312) 715-1234

; TELEX: 910/221-5317

; INFORMATION FOR SEQ ID NO: 44:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2560 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

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; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; NAME/KEY: sig_peptide
; LOCATION: 12..68
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: join(69..435, 712..1005, 1396..1431, 1550..1879,
; LOCATION: 1977..2296)
; FEATURE:
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; LOCATION: 436..711
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1006..1395
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1432..1549
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1880..1976
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "pMDR1002 insert: pre-5A8
; OTHER INFORMATION: humanized heavy chain"
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; FEATURE:
; NAME/KEY: exon
; LOCATION: 712..1005
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1396..1431
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1550..1879
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1977..2296
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(12..435, 712..1005, 1396..1431, 1550..1879,
; LOCATION: 1977..2296)
; US-07-916-098A-44

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Best Local Similarity 89.2%; Pred. No. 0;
Matches 2049; Conservative 0; Mismatches 185; Indels 54; Gaps 7;

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Db      8  CACCATGAGCTGACCTGGAGGCTTCTGCTGCTGTAGCACAGGTGCCACTC 67

Qy      68  CCAGGTCCAGCTGGTGCAGTCTGGGCTGAGTGAAGAGCTCGGAGCTCAGTGAAGGT 127
Db      68  CCAGGTCCAACTGCAGGAGTCTGAGCTGAAGTGAAGAGCTCGGGCTTCAGTGAAGGT 127

Qy      128  GTCTGCAAGGCTTCGGGCTACATTCATCTGATTTATCTATACAGTGGGTGAGACAGGC 187
Db      128  GTCTGCAAGGCTTCGGGATACATTCATCTGATTTATCTATACAGTGGGTGAGCAGGC 187

Qy      188  TCCTGGAAGGGCTTCGAGTGAATTTGAGTTATTAATTTACTATGATATACAACTA 247
Db      188  GCCTGGGAGGGCTTCGAGTGAATTTGAGTTATTAATTTACTATGATATACAACTA 247

Qy      248  CAACAGAGTTTAAGGCGAGGCGACATGACTGTAGACAGTGCAGGAGCAGAGCCTA 307
Db      248  CGATGAGAAGTTCAAAGGCGAGGCGACATGACTGTAGACAGTGCAGGAGCAGAGCCTA 307

Qy      308  TATGGAACCTTAGTTCTTTGAGATCTGAGGATACGGCCGCTTTTATTACTGTGCAAGAG--- 363

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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 08:34:11 ; Search time 92.7113 Seconds

(without alignments)
13047.203 Million cell updates/sec

Title: US-09-627-896b-25

Perfect score: 327

Sequence: 1 gacatccagatgaccagtc.....ccaaggtggaatcaaacgt 327

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2438257 seqs, 1849576744 residues

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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- 2: /cgn2_6/ptodata/1/pubpna/PTCT_NEW_PUB.seq.*
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- 6: /cgn2_6/ptodata/1/pubpna/PTCTUS_PUBCOMB.seq.*
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- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	297.8	91.1	322	14	US-10-041-860-74
2	297.2	90.9	384	15	US-10-309-762-113
3	296.2	90.6	322	14	US-10-041-860-76
4	294	89.9	514	14	US-10-066-543-2025
5	294	89.9	537	14	US-10-066-543-186
6	289.8	88.6	322	14	US-10-041-860-81
7	286	87.5	463	12	US-10-395-894-16
8	286	87.5	6082	12	US-10-395-894-8
9	282	86.2	322	14	US-10-330-613-32
10	282	86.2	322	14	US-10-330-530-32
11	280.6	85.8	717	15	US-10-423-847-9
12	280.2	85.7	747	15	US-10-423-847-7
13	280.2	85.7	750	15	US-10-423-847-3
14	280.2	85.7	750	15	US-10-423-847-6
15	279.6	85.5	741	15	US-10-423-847-4

16	279.6	85.5	756	15	US-10-423-847-1	Sequence 1, Appli
17	279.6	85.5	756	15	US-10-423-847-5	Sequence 5, Appli
18	279.6	85.5	759	15	US-10-423-847-2	Sequence 2, Appli
19	279.6	85.5	762	15	US-10-423-847-8	Sequence 8, Appli
20	279.2	85.4	321	10	US-09-801-185A-36	Sequence 36, Appl
21	279.2	85.4	321	15	US-10-133-715-36	Sequence 36, Appl
22	279.2	85.4	321	15	US-10-302-356A-36	Sequence 36, Appl
23	279.2	85.4	321	15	US-10-163-657A-36	Sequence 36, Appl
24	279.2	85.4	321	15	US-10-422-287-36	Sequence 36, Appl
25	278	85.0	490	10	US-09-918-995-37859	Sequence 37859, A
26	274.8	84.0	737	9	US-09-919-344-7	Sequence 7, Appli
27	274.8	84.0	819	14	US-10-158-646-65	Sequence 65, Appl
28	274.4	83.9	306	14	US-10-010-729-36	Sequence 36, Appl
29	270	82.6	720	9	US-09-192-854-1	Sequence 1, Appli
30	270	82.6	720	9	US-09-968-561A-1	Sequence 1, Appli
31	270	82.6	720	10	US-09-968-744A-1	Sequence 1, Appli
32	270	82.6	720	12	US-09-968-561A-1	Sequence 125, App
33	270	82.6	729	14	US-10-216-484-125	Sequence 125, App
34	270	82.6	729	14	US-10-384-933-125	Sequence 121, App
35	270	82.6	1106	15	US-10-264-049-121	Sequence 20, Appl
36	269	82.3	322	14	US-10-330-613-20	Sequence 20, Appl
37	269	82.3	322	14	US-10-330-530-20	Sequence 68, Appl
38	269	82.3	322	14	US-10-041-860-68	Sequence 70, Appl
39	269	82.3	322	14	US-10-041-860-70	Sequence 78, Appl
40	269	82.3	322	15	US-10-309-762-231	Sequence 231, App
41	269	82.3	322	15	US-10-309-762-235	Sequence 235, App
42	269	82.3	322	14	US-10-041-860-66	Sequence 66, Appl
43	267.4	81.8	322	14	US-10-041-860-66	Sequence 19, Appl
44	266.8	81.6	324	16	US-10-408-901-19	Sequence 43, Appl
45	266.8	81.6	645	16	US-10-408-901-43	

ALIGNMENTS

RESULT 1

US-10-041-860-74
; Sequence 74, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezaheh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 322
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-041-860-74

Query Match 91.1%; Score 297.8; DB 14; Length 322;
Best Local Similarity 96.9%; Pred. No. 1.3e-91;
Matches 315; Conservative 0; Mismatches 7; Indels 3; Gaps 1;

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Db 61 ATCACTTCCCGCGGAGTCAGGCATTAGCAATTTATTAGCTGGTATCAGCAGAAACCA 120

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OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 08:34:11 ; Search time 96.1135 Seconds

(without alignments)
13047.203 Million cell updates/sec

Title: US-09-627-896B-26

Perfect score: 339

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2438257 seqs, 1849576744 residues

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA.*

1: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq.*
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	319.8	94.3	366	14	US-10-010-729-52 Sequence 52, Appl
2	318.2	93.9	357	14	US-10-010-729-14 Sequence 14, Appl
3	316.6	93.4	340	14	US-10-330-613-24 Sequence 24, Appl
4	315.6	93.4	340	14	US-10-330-530-24 Sequence 24, Appl
5	315.2	93.0	463	9	US-09-925-299-453 Sequence 453, Appl
6	315.2	93.0	463	10	US-09-925-299-453 Sequence 453, Appl
7	314	92.6	1028	14	US-10-255-478-67 Sequence 67, Appl
8	314	92.6	1330	14	US-10-255-478-65 Sequence 65, Appl
9	312.4	92.2	1359	14	US-10-255-478-69 Sequence 69, Appl
10	311.8	92.0	792	15	US-10-264-049-2099 Sequence 2099, Ap
11	311.8	92.0	1033	9	US-09-799-514-2 Sequence 2, Appli
12	311.6	91.9	423	14	US-10-390-986-15 Sequence 15, Appl
13	310.2	91.5	804	15	US-10-264-049-2091 Sequence 2091, Ap
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15	305.2	90.0	788	14	US-10-158-646-58 Sequence 58, Appl

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17	301.6	89.0	836	14	US-10-255-478-63	Sequence 63, Appl
18	300.4	88.6	9511	9	US-09-897-006-34	Sequence 34, Appl
19	300.4	88.6	9511	10	US-09-897-006-34	Sequence 34, Appl
20	294.4	86.8	305	10	US-09-995-529-5	Sequence 5, Appli
21	292.6	86.3	342	9	US-09-274-163E-1	Sequence 1, Appli
22	291	85.8	343	9	US-09-274-163E-3	Sequence 3, Appli
23	291	85.8	343	9	US-09-274-163E-5	Sequence 5, Appli
24	291	85.8	1820	15	US-10-104-047-1232	Sequence 1232, Ap
25	289.4	85.4	315	14	US-10-010-729-38	Sequence 38, Appl
26	288	85.0	1230	14	US-10-158-646-59	Sequence 59, Appl
27	287.8	84.9	6094	12	US-10-395-894-13	Sequence 13, Appl
28	281.4	83.0	470	14	US-10-345-618-10	Sequence 10, Appl
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31	280.2	82.7	460	9	US-09-187-693-22	Sequence 22, Appl
32	279	82.3	456	9	US-09-187-693-24	Sequence 24, Appl
33	276.4	81.5	476	9	US-09-187-693-30	Sequence 30, Appl
34	273.4	80.6	384	9	US-09-905-243-54	Sequence 54, Appl
35	272.6	80.4	453	9	US-09-187-693-28	Sequence 28, Appl
36	268.4	79.2	327	9	US-09-828-708-112	Sequence 112, App
37	268.4	79.2	327	9	US-09-828-708-115	Sequence 115, App
38	251.6	74.2	266	9	US-09-604-287A-409	Sequence 409, App
39	251.6	74.2	266	10	US-09-551-621-409	Sequence 409, App
40	251.6	74.2	266	13	US-10-007-805-409	Sequence 409, App
41	251.6	74.2	266	14	US-10-076-622-409	Sequence 409, App
42	251.6	74.2	266	14	US-10-124-805-409	Sequence 409, App
43	246.2	72.6	339	14	US-10-121-464-5	Sequence 5, Appli
44	246.2	72.6	339	14	US-10-159-006-5	Sequence 5, Appli
45	246.2	72.6	339	14	US-10-159-006-103	Sequence 103, App

ALIGNMENTS

RESULT 1

US-10-010-729-52
; Sequence 52, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52

LENGTH: 366

TYPE: DNA

ORGANISM: Homo sapiens

US-10-010-729-52

Query Match 94.3%; Score 319.8; DB 14; Length 366;
Best Local Similarity 96.5%; Pred. No. 5.5e-99;
Matches 327; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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DB 1 GACATCGTGAGACCCAGTCTCCAGACTCCCTGCTGTGTCTCTGGCGAGAGGGCCACC 60
QY 61 ATCAACTGCAAGTCCAGCCAGAGTGTATATACAGTCCCAACAAAGAAATTAATTA 120
DB 61 ATCAACTGCAAGTCCAGCCAGAGTGTATATACAGTCCCAACAAAGAAATTAATTA 120
QY 121 TGGTACCCAGAGAAACAGGACAGCTCCTAAGCTGCTCATTTACTTGGGATCTACCCGG 180
DB 121 TGGTACCCAGAGAAACAGGACAGCTCCTAAGCTGCTCATTTACTTGGGATCTACCCGG 180
QY 181 GAATCCGGGTCCTCCAGCGATTGAGTGGCAGCGGGTCTGGGACAGATTCTCTCACC 240
DB 181 GAATCCGGGTCCTCCAGCGATTGAGTGGCAGCGGGTCTGGGACAGATTCTCTCACC 240
QY 241 ATCAGAGCTGAGGCTGAGATGAGTGGCAGCGGGTCTGGGACAGATTCTCTCACC 300
DB 241 ATCAGAGCTGAGGCTGAGATGAGTGGCAGCGGGTCTGGGACAGATTCTCTCACC 300
QY 301 CCTCGAAGCTTCCGCCAAGGACCAAGGTGGAATCAAA 339
DB 301 CCTCGAAGCTTCCGCCAAGGACCAAGGTGGAATCAAA 339

RESULT 2

US-10-010-729-14
; Sequence 14, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-729-14

Query Match 93.9%; Score 318.2; DB 14; Length 357;
Best Local Similarity 96.2%; Pred. No. 1.9e-98;
Matches 326; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGCTGTGTCTCTGGCGAGAGGGCCACC 60
DB 1 GACATCGTGAGACCCAGTCTCCAGACTCCCTGCTGTGTCTCTGGCGAGAGGGCCACC 60
QY 61 ATCAACTGCAAGTCCAGCCAGAGTGTATATACAGTCCCAACAAAGAAATTAATTA 120
DB 61 ATCAACTGCAAGTCCAGCCAGAGTGTATATACAGTCCCAACAAAGAAATTAATTA 120
QY 121 TGGTACCCAGAGAAACAGGACAGCTCCTAAGCTGCTCATTTACTTGGGATCTACCCGG 180

DB 121 TGGTACCCAGAGAAACAGGACAGCTCCTAAGCTGCTCATTTACTTGGGATCTACCCGG 180
QY 181 GAATCCGGGTCCTCCAGCGATTGAGTGGCAGCGGGTCTGGGACAGATTCTCTCACC 240
DB 181 GAATCCGGGTCCTCCAGCGATTGAGTGGCAGCGGGTCTGGGACAGATTCTCTCACC 240
QY 241 ATCAGAGCTGAGGCTGAGATGAGTGGCAGCGGGTCTGGGACAGATTCTCTCACC 300
DB 241 ATCAGAGCTGAGGCTGAGATGAGTGGCAGCGGGTCTGGGACAGATTCTCTCACC 300
QY 301 CCTCGAAGCTTCCGCCAAGGACCAAGGTGGAATCAAA 339
DB 301 CCTCGAAGCTTCCGCCAAGGACCAAGGTGGAATCAAA 339

RESULT 3

US-10-330-613-24
; Sequence 24, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 340
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-24

Query Match 93.4%; Score 316.6; DB 14; Length 340;
Best Local Similarity 95.9%; Pred. No. 6.7e-98;
Matches 325; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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DB 1 GACATCGTGAGACCCAGTCTCCAGACTCCCTGCTGTGTCTCTGGCGAGAGGGCCACC 60
QY 61 ATCAACTGCAAGTCCAGCCAGAGTGTATATACAGTCCCAACAAAGAAATTAATTA 120
DB 61 ATCAACTGCAAGTCCAGCCAGAGTGTATATACAGTCCCAACAAAGAAATTAATTA 120
QY 121 TGGTACCCAGAGAAACAGGACAGCTCCTAAGCTGCTCATTTACTTGGGATCTACCCGG 180
DB 121 TGGTACCCAGAGAAACAGGACAGCTCCTAAGCTGCTCATTTACTTGGGATCTACCCGG 180
QY 181 GAATCCGGGTCCTCCAGCGATTGAGTGGCAGCGGGTCTGGGACAGATTCTCTCACC 240
DB 181 GAATCCGGGTCCTCCAGCGATTGAGTGGCAGCGGGTCTGGGACAGATTCTCTCACC 240
QY 241 ATCAGAGCTGAGGCTGAGATGAGTGGCAGCGGGTCTGGGACAGATTCTCTCACC 300
DB 241 ATCAGAGCTGAGGCTGAGATGAGTGGCAGCGGGTCTGGGACAGATTCTCTCACC 300
QY 301 CCTCGAAGCTTCCGCCAAGGACCAAGGTGGAATCAAA 339
DB 301 CCTCGAAGCTTCCGCCAAGGACCAAGGTGGAATCAAA 339

RESULT 4

US-10-330-530-24
; Sequence 24, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 08:27:41 ; Search time 19.7311 Seconds
(without alignments)
9534.601 Million cell updates/sec

Title: US-09-627-896B-26

Perfect score: 339

Sequence: 1 gacatccagtgaccagtc.....ggaccaaggtggaatcaaa 339

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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2: /cgn2_6/ptodata/2/ina/5B COMB.seq:*

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4: /cgn2_6/ptodata/2/ina/6B COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	321.4	94.8	342	1	US-08-360-125-4
2	321.4	94.8	342	2	US-08-450-578-4
3	321.4	94.8	342	2	US-09-017-628-4
4	321.4	94.8	342	2	US-09-014-880-4
5	321.4	94.8	342	4	US-08-450-363-4
6	319.4	94.1	360	1	US-08-026-320A-3
7	314.9	92.6	1028	4	US-08-961-309-67
8	314.9	92.6	1330	3	US-08-463-903-5
9	314.9	92.6	1330	4	US-07-935-695-5
10	314.9	92.6	1330	4	US-08-961-309-65
11	312.4	92.2	1027	3	US-08-463-903-19
12	312.4	92.2	1027	4	US-07-935-695-19
13	312.4	92.2	1359	4	US-08-961-309-69
14	311.6	91.9	423	4	US-09-582-337-15
15	310.2	91.5	1088	4	US-08-961-309-57
16	309.2	91.2	1361	3	US-08-463-903-21
17	309.2	91.2	1361	4	US-07-935-695-21
18	308.6	91.0	1088	3	US-08-463-903-3
19	308.6	91.0	1088	4	US-07-935-695-3
20	301.6	89.0	836	3	US-08-463-903-1
21	301.6	89.0	836	4	US-07-935-695-1
22	301.6	89.0	836	4	US-08-961-309-63
23	292.6	86.3	342	4	US-09-274-163B-1
24	292.4	86.3	302	3	US-08-724-752-6
25	292.4	86.3	302	4	US-08-923-138-14
26	291.8	85.8	343	4	US-09-274-163E-3
27	291.8	85.8	343	4	US-09-274-163E-5

28 284 83.8 470 3 US-08-724-752-13 Sequence 13, Appl
29 281.4 83.0 470 3 US-08-828-741B-10 Sequence 10, Appl
30 281.4 83.0 470 4 US-08-160-567-10 Sequence 10, Appl
31 281.4 83.0 470 4 US-09-710-299-10 Sequence 10, Appl
32 281.4 83.0 470 4 US-09-509-031-10 Sequence 10, Appl
33 281.4 83.0 1031 3 US-08-828-741B-5 Sequence 5, Appl
34 281.4 83.0 1031 4 US-09-160-567-5 Sequence 5, Appl
35 281.4 83.0 1031 4 US-09-710-299-5 Sequence 5, Appl
36 281.4 83.0 1031 4 US-09-509-031-5 Sequence 5, Appl
37 281.4 83.0 1490 3 US-08-828-741B-3 Sequence 3, Appl
38 281.4 83.0 1490 4 US-09-160-567-3 Sequence 3, Appl
39 281.4 83.0 1490 4 US-09-710-299-3 Sequence 3, Appl
40 281.4 83.0 1490 4 US-09-509-031-3 Sequence 3, Appl
41 268.6 79.2 339 5 PCT-US93-08435-7 Sequence 7, Appl
42 267 78.8 339 5 PCT-US93-08435-5 Sequence 5, Appl
43 254.2 75.0 339 1 US-08-467-420A-20 Sequence 20, Appl
44 254.2 75.0 339 1 US-08-470-110A-20 Sequence 20, Appl
45 254.2 75.0 339 1 US-08-667-769A-20 Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-360-125-4
; Sequence 4, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Yoshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,125
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:

INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna

GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5837845ihiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-4

Query Match 94.8%; Score 321.4; DB 1; Length 342;
Best Local Similarity 96.8%; Pred. No. 9.4e-98;
Matches 328; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Db 1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGCGGAGGGCCACC 60
QY 61 ATCAACTGCAAGTCCAGCCAGAGTGTATATACAGCTCCCAACAAGAATTAATTAACT 120
Db 61 ATCAACTGCAAGTCCAGCCAGAGTGTATATACAGCTCCCAACAAGAATTAATTAGCT 120
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Db 121 TGGTACCAGCAGAAACCCAGGACAGCTCTTAAGCTGCTCAATTTACTGGGCATCTACCCGG 180
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Db 181 GAATCCGGGGTCCCTGACCGATTGAGTGGGAGCGGGTCTGGGACAGATTTCACTCTCACC 240
QY 241 ATCAGCAGCTGCGAGGCTGAAGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
Db 241 ATCAGCAGCTGCGAGGCTGAAGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
QY 301 CCTCGAAGCTTGGCCAGAGGACCAAGCTGGAATCAAA 339
Db 301 CCGTGGACGTTCCGGCCAGAGGACCAAGCTGGAATCAAA 339

RESULT 2
US-08-450-578-4
; Sequence 4, Application US/08450578
; Patent No. 5837845

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 08:34:11 ; Search time 104.336 Seconds
(without alignments)
13047.203 Million cell updates/sec

Title: US-09-627-896B-29
Perfect score: 368
Sequence: 1 aggtgcagcgtgcagtct.....ccctgtcatgtctctctca 368

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Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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- 3: /cgn2_6/ptodata/1/pubna/US06_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubna/US07_NEW_PUB.seq:*
- 5: /cgn2_6/ptodata/1/pubna/PCTUS_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubna/US08_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/1/pubna/US09_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubna/US10A_PUBCOMB.seq:*
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- 15: /cgn2_6/ptodata/1/pubna/US10_NEW_PUB.seq:*
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- 18: /cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	285.2	77.5	1431	15	US-10-461-148-8
3	284.8	77.4	354	14	US-10-300-675-5
4	284.8	77.4	354	14	US-10-300-675-9
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6	283.2	77.0	354	14	US-10-300-675-11
7	277.6	75.4	495	9	US-09-925-299-92
8	277.6	75.4	495	10	US-10-151-882-9
9	276.8	75.2	723	14	US-10-091-300-19
10	276	75.0	375	14	US-10-091-300-19
11	274	74.5	1599	9	US-09-954-456-789
12	274	74.5	1599	9	US-09-954-456-1604
13	274	74.5	1599	10	US-09-960-706-704
14	274	74.5	1599	10	US-09-873-319-445
15	274	74.5	1599	10	US-09-873-367C-1010

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27	263.6	71.6	717	14	US-10-151-882-11
28	263.6	71.6	744	14	US-10-151-882-7
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ALIGNMENTS

RESULT 1

US-10-225-108A-15
; Sequence 15, Application US/10225108A
; Publication No. US20030157112A1
; GENERAL INFORMATION:
; APPLICANT: HOOPER, Craig
; APPLICANT: DIETZSCHOLD, Bernhard
; TITLE OF INVENTION: Recombinant Antibodies, and Compositions
; TITLE OF INVENTION: and Methods for Making Them
; FILE REFERENCE: 8321-110
; CURRENT APPLICATION NUMBER: US/10/225,108A
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/848,832
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/204,518
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-108A-15

Query Match 77.5%; Score 285.2; DB 14; Length 1431;
Best Local Similarity 86.8%; Pred. No. 2.7e-86;
Matches 330; Conservative 0; Mismatches 38; Indels 12; Gaps 1;

QY	1	AGGTGAGCTGCTGCAGTCTGGGGTGGAGGCTGAAGAGCTGGTCTCGTAAAGTCT 60
DB	59	AGGTGAGCTGCTGCAGTCTGGGGTGGAGGCTGAAGAGCTGGTCTCGTAAAGTCT 118
QY	61	CTGCAAGCTTCTGGAGGCACCTTCAGTACTATCTACTATCTAGCTGGTGGCAGGCCC 120
DB	119	CTGCAAGCTTCTGGAGGCACCTTCAGTACTATCTACTATCTAGCTGGTGGCAGGCCC 178

QY 121 CTGCAAGAGGCTTGGTGGATGGAGGATCATGCTATCCTTGGACTAGCAAAATTACG 180
Db 179 CTGCAAGAGGCTTGGTGGATGGAGGATCATCCTCTCTTTGGTACGAAATACG 238
QY 181 CACAGAGTTCCAGGGCAGAGTCAAGATTACCGGGACAAATCCACGAGCACAGCTTACA 240
Db 239 CACAGAGTTCCAGGGCAGAGTCAAGATTACCGGGACAAATCCACGAGCACAGCTTACA 298
QY 241 TGGAGCTGACAGCTCAGATCTGAGGACAGGCGCGTGTATTACTGTGCGAGATCCCG 300
Db 299 TGGAGCTGACAGCTCAGATCTGATGACAGGCGCGTGTATTCTGTGCGAGAGAAATC 358
QY 301 ATTATGTTGGGGAGGAGCAAA-----CTGTTTCGACCCCTGGGGCCAGGGAA 348
Db 359 TCGTAAATTCGGGAGCTATTATTTCTCAGGCTGGTTCGACCCCTGGGGCCAGGGAA 418
QY 349 CCCTGCTCATCGTCTCTCA 368
Db 419 CCCTGGTCAACGGTCTCTCA 438

RESULT 2

US-10-461-148-8
; Sequence 8, Application US/10461148
; Publication No. US20040013672A1
; GENERAL INFORMATION:
; APPLICANT: Dietzschold, Bernhard
; APPLICANT: Hooper, Douglas C.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND COMPOSITIONS
; FILE REFERENCE: 8321-110C11-185685
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US/10/461,148
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/849,832
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/204,518
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Human
US-10-461-148-8

Query Match 77.5%; Score 285.2; DB 15; Length 1431;
Best Local Similarity 86.8%; Pred. No. 2.7e-86;
Matches 330; Conservative 0; Mismatches 38; Indels 12; Gaps 1;
QY 1 AGGTGACGCTGGTCACTTGGGCTCAGGTGAAGAGCCTGGTCTCTCGGTAAAGTCT 60
Db 59 AGGTGACGCTGGTCACTTGGGCTCAGGTGAAGAGCCTGGTCTCTCGGTAAAGTCT 118
QY 61 CCTGCAAGGCTTCTGGAGGACCTTCAAGTATTACTATCATCAGCTGGGTGCGACAGGCC 120
Db 119 CCTGCAAGGCTTCTGGAGGACCTTCAAGTATTACTATCATCAGCTGGGTGCGACAGGCC 178
QY 121 CTGCAAGGCTTGGTGGATGGAGGATCATGCTATCCTTGGACTAGCAAAATTACG 180
Db 179 CTGCAAGGCTTGGTGGATGGAGGATCATCCTCTATCTTTGGTACGAAATACG 238
QY 181 CACAGAGTTCCAGGGCAGAGTCAAGATTACCGGGACAAATCCACGAGCACAGCTTACA 240
Db 239 CACAGAGTTCCAGGGCAGAGTCAAGATTACCGGGACAAATCCACGAGCACAGCTTACA 298
QY 241 TGGAGCTGACAGCTCAGATCTGAGGACAGGCGCGTGTATTACTGTGCGAGATCCCG 300
Db 299 TGGAGCTGACAGCTCAGATCTGATGACAGGCGCGTGTATTCTGTGCGAGAGAAATC 358

QY 301 ATTATGTTGGGGAGGAGCAAA-----CTGTTTCGACCCCTGGGGCCAGGGAA 348
Db 359 TCGTAAATTCGGGAGCTATTATTTCTCAGGCTGGTTCGACCCCTGGGGCCAGGGAA 418
QY 349 CCCTGCTCATCGTCTCTCA 368
Db 419 CCCTGGTCAACGGTCTCTCA 438

RESULT 3

US-10-300-675-5
; Sequence 5, Application US/10300675
; Publication No. US20030198638A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffery D.
; TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
; FILE REFERENCE: P-IX 5519
; CURRENT APPLICATION NUMBER: US/10/300,675
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 09/989,901
; PRIOR FILING DATE: 2001-11-19
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(354)
US-10-300-675-5

Query Match 77.4%; Score 284.8; DB 14; Length 354;
Best Local Similarity 88.6%; Pred. No. 2.5e-86;
Matches 326; Conservative 0; Mismatches 27; Indels 15; Gaps 1;

QY 1 AGGTGACGCTGGTGCAGTCTTGGGGCTGAGGTGAAGAGCCTGGGTCTCTCGGTAAAGTCT 60
Db 2 AGGTGACGCTGGTGCAGTCTTGGGGCTGAGGTGAAGAGCCTGGGTCTCTCGGTAAAGTCT 61
QY 61 CTGCAAGGCTTCTGGAGGACCTTCAAGTATTACTATCATCAGCTGGGTGCGACAGGCC 120
Db 62 CTGCAAGGCTTCTGGAGGACCTTCAAGTATTACTATCATCAGCTGGGTGCGACAGGCC 121
QY 121 CTGCAAGGCTTGGTGGATGGAGGATCATGCTATCCTTGGACTAGCAAAATTACG 180
Db 122 CTGCAAGGCTTGGTGGATGGAGGATCATCCTATCTTTGGTACGAAATACG 181
QY 181 CACAGAGTTCCAGGGCAGAGTCAAGATTACCGGGACAAATCCACGAGCACAGCTTACA 240
Db 182 CACAGAGTTCCAGGGCAGAGTCAAGATTACCGGGACAAATCCACGAGCACAGCTTACA 241
QY 241 TGGAGCTGACAGCTCAGATCTGAGGACAGGCGCGTGTATTACTGTGCGAGATCCCG 300
Db 242 TGGAGCTGACAGCTCAGATCTGAGGACAGGCGCGTGTATTACTGTGCGAGAGAGAG 296
QY 301 ATTATGTTGGGGAGGAGCAACTGTTTCGACCCCTGGGGCCAGGGAAACCTCTCATCG 360
Db 297 -----AGATAGCAGTGGCTGGTATCATTCTACTTGGGCCAGGGAAACCTCTCATCG 346
QY 361 TCTCTCA 368
Db 347 TCTCTCA 354

RESULT 4

US-10-300-675-9
; Sequence 9, Application US/10300675
; Publication No. US20030198638A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffery D.
; TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
; FILE REFERENCE: P-IX 5519

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 08:27:41 ; Search time 21.419 seconds
(without alignments)
9534.601 Million cell updates/sec

Title: US-09-627-896B-29
Perfect score: 368
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Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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2: /cgn2_6/prodata/2/ina/5B COMB.seq.*
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4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCUTUS COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	293.2	79.7	2287	1	US-08-480-036-1
2	293.2	79.7	2287	1	US-08-461-968A-1
3	293.2	79.7	2287	2	US-08-462-571-1
4	293.2	79.7	2287	4	US-08-472-888A-1
5	293.2	79.7	2287	5	PCT-US96-10043-8
6	282.4	76.7	369	2	US-08-652-816A-46
7	280.8	76.3	369	2	US-08-652-816A-44
8	280.8	76.3	812	2	US-07-834-539A-53
9	280.8	76.3	812	2	US-08-800-353-53
10	280.8	76.3	812	3	US-09-042-353-231
11	280.8	76.3	812	4	US-08-758-417A-79
12	280.8	76.3	812	5	PCT-US92-06185-53
13	280.8	76.3	813	1	US-08-053-131-61
14	280.8	76.3	813	1	US-08-645-641-61
15	280.8	76.3	813	1	US-07-853-408B-61
16	280.8	76.3	813	1	US-08-086-762-61
17	280.8	76.3	813	2	US-08-308-865-61
18	280.8	76.3	813	5	PCT-US92-10983-61
19	279.2	75.9	369	2	US-08-652-816A-45
20	277.6	75.4	369	2	US-08-652-816A-47
21	277.4	75.4	454	4	US-09-220-132-98
22	274	74.5	1599	4	US-09-023-655-1120
23	272.8	74.1	369	2	US-08-652-816A-25
24	272.4	74.0	1617	2	US-08-378-939-9
25	250.4	68.0	4691	3	US-08-591-632-43
26	250.4	68.0	4691	4	US-09-611-451-43
27	250.4	68.0	6166	3	US-08-591-632-51

28 250.4 68.0 6166 4 US-09-611-451-51 Sequence 51, Appl
29 250.2 68.0 441 1 US-08-217-918-3 Sequence 3, Appl
30 248.4 67.5 372 4 US-08-635-109-15 Sequence 15, Appl
31 248 67.4 687 1 US-08-300-386A-1 Sequence 1, Appl
32 248 67.4 687 3 US-08-931-645-1 Sequence 1, Appl
33 248 67.4 687 5 PCT-US94-01258-1 Sequence 1, Appl
34 248 67.4 687 5 PCT-US95-11235-1 Sequence 1, Appl
35 243.6 66.2 363 1 US-08-264-093-1 Sequence 1, Appl
36 236.4 64.2 564 3 US-08-545-809A-8 Sequence 8, Appl
37 236 64.1 539 3 US-08-545-809A-18 Sequence 18, Appl
38 234.4 63.7 799 3 US-08-545-809A-46 Sequence 46, Appl
39 233.2 63.4 246 3 US-09-042-353-146 Sequence 146, App
40 233.2 63.4 246 4 US-08-758-417A-410 Sequence 410, App
41 232.8 63.3 936 3 US-09-049-672A-26 Sequence 26, Appl
42 231.2 62.8 512 3 US-08-545-809A-2 Sequence 2, Appl
43 230 62.5 395 1 US-08-482-882-85 Sequence 85, Appl
44 230 62.5 395 1 US-08-483-389-85 Sequence 85, Appl
45 230 62.5 395 2 US-08-487-113D-85 Sequence 85, Appl

ALIGNMENTS

RESULT 1
US-08-480-036-1
; Sequence 1, Application US/08480036
; Patent No. 5723583
; GENERAL INFORMATION:
; APPLICANT: Seed, Brian et al.
; TITLE OF INVENTION: INHIBITION OF CELL ADHESION
; TITLE OF INVENTION: PROTEIN-CARBOHYDRATE
; INTERACTIONS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.00)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,036
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/618,314C
; FILING DATE: No. 5723583ember 23, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/067001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2287
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-480-036-1

Query Match 79.7%; Score 293.2; DB 1; Length 2287;
Best Local Similarity 88.2%; Pred. No. 3.7e-86;
Matches 395; Conservative 0; Mismatches 33; Indels 12; Gaps 1;
1 AGGTGCAGCTGCTGTCAGTCTGGGGCTGAGGTGAAGAGCCTGGGTCTCTCGTAAGGTCT 60

Db 74 AGGTGACGCTGGTGCAGTCTGGGGCTGAGTGAGAGGCTGGTCTCGGTGAGGTCT 133
QY 61 CTTGCAAGGCTTCTTGAGGACACCTTCAGTAGTTATATCACTAGCTGGTGCACAGGCC 120
Db 134 CTTGCAAGGCTTCTTGAGGACACCTTCAGTAGTTATATCACTAGCTGGTGCACAGGCC 193
QY 121 CTGGCAAGGCTTCTTGAGTGGATGGGAGGATCATGCTATCTTGTGACTAGCAAAATACG 180
Db 194 CTGGCAAGGCTTCTTGAGTGGATGGGAGGATCATGCTATCTTGTGACTAGCAAAATACG 253
QY 181 CACAGAGGTTCCAGGGCAGAGTCACGATTACCGCGACAAATCCACGAGCACGCTTACA 240
Db 254 CACAGAGGTTCCAGGGCAGAGTCACGATTACCGCGACAAATCCACGAGCACGCTTACA 313
QY 241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCCGTGTATTACTGTGGAGAGATCCCG 300
Db 314 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCCGTGTATTACTGTGGAGAGATAATG 373
QY 301 -----ATTATGTTTGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAA 348
Db 374 GAGCGTATTGTAGTGGTAGTCTGCTACTCGGGCTGGTTCGACCCCTGGGGCCAGGGAA 433
QY 349 CCTGCTCATCGTCTCTTCA 368
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RESULT 2

US-08-461-968A-1
; Sequence 1, Application US/08461968A
; Patent No. 5801044
; GENERAL INFORMATION:
; APPLICANT: Seed et al., Brian
; TITLE OF INVENTION: INHIBITION OF CELL ADHESION
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 0210-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,968A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/618,314
; FILING DATE: 23-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/067003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2287
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-461-968A-1

Query Match

79.7%; Score 293.2; DB 1; Length 2287;

Best Local Similarity 88.2%; Pred. No. 3.7e-86;
Matches 335; Conservative 0; Mismatches 33; Indels 12; Gaps 1;
QY 1 AGGTGACGCTGGTGCAGTCTGGGGCTGAGGTGAGAGGCTGGTCTCGGTAAAGGTCT 60
Db 74 AGGTGACGCTGGTGCAGTCTGGGGCTGAGGTGAGAGGCTGGTCTCGGTAAAGGTCT 133
QY 61 CTTGCAAGGCTTCTTGAGGACACCTTCAGTAGTTATATCACTAGCTGGTGCACAGGCC 120
Db 134 CTTGCAAGGCTTCTTGAGGACACCTTCAGTAGTTATATCACTAGCTGGTGCACAGGCC 193
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QY 181 CACAGAGGTTCCAGGGCAGAGTCACGATTACCGCGACAAATCCACGAGCACGCTTACA 240
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QY 241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCCGTGTATTACTGTGGAGAGATCCCG 300
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QY 301 -----ATTATGTTTGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAA 348
Db 374 GAGCGTATTGTAGTGGTAGTCTGCTACTCGGGCTGGTTCGACCCCTGGGGCCAGGGAA 433
QY 349 CCTGCTCATCGTCTCTTCA 368
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RESULT 3

US-08-462-571-1
; Sequence 1, Application US/08462571
; Patent No. 5858983
; GENERAL INFORMATION:
; APPLICANT: Seed, Brian et al.
; TITLE OF INVENTION: INHIBITION OF CELL ADHESION
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55X
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,571
; FILING DATE: 05 June 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/618,314
; FILING DATE: 23 No. 5858983ember 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/067002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2287
; TYPE: nucleic acid
; STRANDEDNESS: single

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 08:34:11 ; Search time 101.5 Seconds
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13047.203 Million cell updates/sec

Title: US-09-627-896B-30
Perfect score: 358
Sequence: 1 gtgcagctgggtgagctctgg.....ccctggtcacgctctctca 358

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	243.8	68.1	357	14	US-10-120-377-72
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5	243.8	68.1	414	15	US-10-309-764-130
6	243	67.9	675	10	US-09-453-234-67
7	242.2	67.7	414	15	US-10-309-764-134
8	241.6	67.5	732	14	US-10-322-673-60
9	241	67.3	402	9	US-09-811-737-7
10	241	67.3	788	9	US-09-811-737-24
11	240.6	67.2	414	14	US-10-401-344-5
12	240.6	67.2	2002	14	US-10-401-344-1
13	240	67.0	939	13	US-10-052-798-7
14	240	67.0	939	14	US-10-288-917-7
15	240	67.0	939	15	US-10-423-448-7

16	239.4	66.9	354	14	US-10-120-377-74
17	239	66.8	294	10	US-09-995-529-7
18	239	66.8	414	15	US-10-309-764-126
19	237.6	66.4	672	10	US-09-972-656-67
20	237.4	66.3	294	15	US-10-338-366-51
21	237.4	66.3	1395	14	US-10-153-382-8
22	237	66.2	348	14	US-10-324-493-15
23	236.8	66.1	1736	15	US-10-291-265-98
24	236.2	66.0	354	15	US-10-173-551-13
25	236	65.9	375	14	US-10-172-317-1
26	236	65.9	375	14	US-10-320-094-1
27	233.6	65.3	1741	15	US-10-291-265-97
28	233	65.1	1392	14	US-10-153-382-1
29	233	65.1	1392	14	US-10-153-382-4
30	233	65.1	1392	14	US-10-153-382-12
31	233	65.1	1999	14	US-10-153-382-2
32	233	65.1	5925	14	US-10-235-175-78
33	232.2	64.9	405	15	US-10-309-764-58
34	232.2	64.9	405	15	US-10-309-764-70
35	231.4	64.6	354	14	US-10-324-493-7
36	231.4	64.6	379	14	US-10-041-860-55
37	231	64.5	357	14	US-10-073-644C-1
38	231	64.5	630	9	US-09-844-684-14
39	231	64.5	630	14	US-10-040-244-14
40	230.6	64.4	348	15	US-10-338-366-1
41	230.6	64.4	9182	10	US-09-927-122-41
42	230.6	64.4	9182	10	US-09-927-121B-89
43	230.2	64.3	675	10	US-09-453-234-59
44	230.2	64.3	675	10	US-09-453-234-91
45	230.2	64.3	677	10	US-09-453-234-55

ALIGNMENTS

RESULT 1

US-10-322-673-63
; Sequence 63, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 63
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding CM013F04 scFv
US-10-322-673-63

Query Match 74.5%; Score 266.6; DB 14; Length 741;
Best Local Similarity 88.2%; Pred. No. 3.6e-80;
Matches 313; Conservative 0; Mismatches 39; Indels 3; Gaps 2;
1 GTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
|||||

Db 4 GTGACGTGTGGAGTCCGGGGAGGCTTGGTCCAGCCTGGGGGTCCCTGAGACTTCC 63
QY 61 TGTGACGCTTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTAGCCAGGCTCCA 119
Db 64 TGTGACGCTTCGTGATTCACCTTTAGTGTATTTGATGAGCTGGGTCCGCGAGGCTCCA 123
QY 120 GGAAGGGGCTGGAGTGGGTGGTAAATATATATGATGAGTGGGAATGAACCATATATGG 179
Db 124 GGAAGGGGCTGGAGTGGGTGGTAAATATATGATGAGTGGGAATGAACCATATATGG 183
QY 180 GACTCTGTGAAGGGCGGATTCACATCTCCAGAGGCAACCCAGAACTCACTGTATCTG 239
Db 184 GACTCTGTGAAGGGCGGATTCACATCTCCAGAGGCAACCCAGAACTCACTGTATCTG 243
QY 240 CAAATGAACAGCCTGAGAGCGGAGGACACGCGCTGTATTTACTGTGGAGGGATCTGT 299
Db 244 CAAATGAACAGCCTGAGAGCGGAGGACACGCGCTGTATTTACTGTGGAGGGATCTGT 301
QY 300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGAAACCCCTGGTCAACGCTTC 354
Db 302 CTGGCTACGCTGACTACTTTGACTACTGGGGCCAGGCAACCCCTGGTCAACGCTTC 356

RESULT 2

US-10-010-729-50
; Sequence 50, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-729-50

Query Match 69.0%; Score 247; DB 14; Length 372;
Best Local Similarity 83.5%; Pred. No. 1.3e-73;
Matches 308; Conservative 0; Mismatches 50; Indels 11; Gaps 2;
QY 1 GTGACGTGTGGAGTCTGGGGAGGCTTGGTCCAGCCTGGAGGGTCCCTGAGACTTCC 60
Db 4 GTGACGTGTGGAGTCTGGGGAGGCTTGGTCCAGCCTGGGGGTCCCTGAGACTTCC 63
QY 61 TGTGACGCTTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTAGCCAGGCTCCA 119
Db 64 TGTGACGCTTCGTGATTCACCTTTAGTGTATTTGATGAGCTGGGTCCGCGAGGCTCCA 123
QY 120 GGAAGGGGCTGGAGTGGGTGGTAAATATATATGATGAGTGGGAATGAACCATATATGG 179
Db 124 GGAAGGGGCTGGAGTGGGTGGTAAATATATGATGAGTGGGAATGAACCATATATGG 183

QY 180 GACTCTGTGAAGGGCGGATTCACATCTCCAGAGGCAACCCAGAACTCACTGTATCTG 239
Db 184 GACTCTGTGAAGGGCGGATTCACATCTCCAGAGGCAACCCAGAACTCACTGTATCTG 243
QY 240 CAAATGAACAGCCTGAGAGCGGAGGACACGCGCTGTATTTACTGTGGAGGAGGAGG 290
Db 244 CAAATGAACAGCCTGAGAGCGGAGGACACGCGCTGTATTTACTGTGGAGGAGGAGG 303
QY 291 -GGGATCTCTTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGAAACCCCTGGTCAAC 349
Db 304 GGTGGTGTACTGTCTTTTACCATGTGTCTGTGGGGCGGTGGCACCCCTGGTCACT 363
QY 350 GTCTCTCTCA 358
Db 364 GTCTCTCTCA 372

RESULT 3

US-10-120-377-72
; Sequence 72, Application US/10120377
; Publication No. US20030176674A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig, et al.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
; FILE REFERENCE: PF112P8
; CURRENT APPLICATION NUMBER: US/10/120,377
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/283,391
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/317,600
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 72
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-120-377-72

Query Match 68.1%; Score 243.8; DB 14; Length 357;
Best Local Similarity 83.8%; Pred. No. 1.6e-72;
Matches 301; Conservative 0; Mismatches 52; Indels 6; Gaps 2;

QY 1 GTGACGTGTGGAGTCTGGGGAGGCTTGGTCCAGCTGGAGGGTCCCTGAGACTTCC 60
Db 4 GTGACGTGTGGAGTCTGGGGAGGCTTGGTCCAGCTGGAGGGTCCCTGAGACTTCC 63
QY 61 TGTGACGCTTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTAGCCAGGCTCCA 119
Db 64 TGTGACGCTTCGTGATTCACCTTTAGTGTATTTGATGAGCTGGGTCCGCGAGGCTCCA 123
QY 120 GGAAGGGGCTGGAGTGGGTGGTAAATATATATGATGAGTGGGAATGAACCATATATGG 179
Db 124 GGAAGGGGCTGGAGTGGGTGGTAAATATATGATGAGTGGGAATGAACCATATATGG 183
QY 180 GACTCTGTGAAGGGCGGATTCACATCTCCAGAGGCAACCCAGAACTCACTGTATCTG 239
Db 184 GACTCTGTGAAGGGCGGATTCACATCTCCAGAGGCAACCCAGAACTCACTGTATCTG 243
QY 240 CAAATGAACAGCCTGAGAGCGGAGGACACGCGCTGTATTTACTGTGGAGGGAGTCTGT 299
Db 244 CAAATGAACAGCCTGAGAGCGGAGGACACGCGCTGTATTTACTGTGGAGGAGGAGG 298
QY 300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGAAACCCCTGGTCAACGCTTCCTCA 358
Db 299 GGTGGTGTGGTCTGTTTGTACTACTGGGGCCAGGAAACCCCTGGTCAACGCTTCCTCA 357

RESULT 4

US-10-010-729-8
; Sequence 8, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 08:27:41 ; Search time 20.837 Seconds
(without alignments)
9534.601 Million cell updates/sec

Title: US-09-627-896B-30

Perfect score: 358

Sequence: 1 gtgcagctgtggagtgctgg.....ccctgtgcaacgctctctca 358

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/FACTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	243	67.9	675	4	US-09-456-090A-67
2	240	67.0	877	3	US-08-545-809A-7
3	240	67.0	939	4	US-09-079-029-7
4	237.4	66.3	1395	4	US-09-472-087-28
5	237.4	66.3	1395	4	US-09-472-087-57
6	233	65.1	1392	4	US-09-472-087-27
7	233	65.1	1392	4	US-09-472-087-30
8	233	65.1	1392	4	US-09-472-087-53
9	233	65.1	1392	4	US-09-472-087-55
10	233	65.1	1392	4	US-09-472-087-59
11	233	65.1	1999	4	US-09-472-087-54
12	233	65.1	5925	4	US-09-315-926A-78
13	230.2	64.3	675	4	US-09-456-090A-59
14	230.2	64.3	675	4	US-09-456-090A-91
15	230.2	64.3	677	3	US-09-456-090A-55
16	228	63.7	375	3	US-09-240-274-89
17	226.4	63.2	375	3	US-09-240-274-90
18	225.8	63.1	1350	1	US-08-157-101A-9
19	225.8	63.1	1576	1	US-08-157-101A-6
20	225.4	63.0	375	3	US-09-240-274-91
21	225.4	63.0	675	4	US-09-456-090A-107
22	224.8	62.8	375	3	US-09-240-274-77
23	223.8	62.5	675	4	US-09-456-090A-105
24	223.6	62.5	381	3	US-09-240-274-88
25	223.4	62.4	354	2	US-08-652-816A-22
26	223	62.3	363	3	US-09-202-181-3
27	222.6	62.2	432	1	US-08-026-320A-1

28	222.2	62.1	675	4	US-09-456-090A-61	Sequence 61, Appl
29	222.2	62.1	675	4	US-09-456-090A-69	Sequence 69, Appl
30	222.2	62.1	675	4	US-09-456-090A-99	Sequence 99, Appl
31	222.2	62.1	675	4	US-09-456-090A-101	Sequence 101, Appl
32	222.2	62.1	675	4	US-09-456-090A-109	Sequence 109, Appl
33	222.2	62.1	892	4	US-09-273-839A-11	Sequence 11, Appl
34	221.6	61.9	375	3	US-09-240-274-92	Sequence 92, Appl
35	220.6	61.6	675	4	US-09-456-090A-57	Sequence 57, Appl
36	220.6	61.6	675	4	US-09-456-090A-93	Sequence 93, Appl
37	220.4	61.6	381	3	US-09-240-274-87	Sequence 87, Appl
38	219.4	61.3	360	2	US-08-428-197-21	Sequence 21, Appl
39	219.4	61.3	360	5	PCT-US93-10555-21	Sequence 21, Appl
40	218.4	61.0	363	3	US-08-599-226-37	Sequence 37, Appl
41	218.4	61.0	363	3	US-09-125-098-37	Sequence 37, Appl
42	218.4	61.0	363	4	US-09-540-018-37	Sequence 37, Appl
43	218.4	61.0	1413	4	US-09-472-087-61	Sequence 61, Appl
44	217.8	60.8	360	2	US-08-428-197-19	Sequence 19, Appl
45	217.8	60.8	360	2	US-08-958-201-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-09-456-090A-67
; Sequence 67, Application US/09456090A
; Patent No. 6680209

GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars

; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils

; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US

; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06

; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 67

; LENGTH: 675

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(675)

; OTHER INFORMATION: M1-23H

US-09-456-090A-67

Query Match 67.9%; Score 243; DB 4; Length 675;
Best Local Similarity 84.1%; Pred. No. 5.5e-65;
Matches 302; Conservative 0; Mismatches 45; Indels 12; Gaps 2;

QY	1	GTGCACTGGTGGAGCTCTGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC	60
Db	4	GTGCACTGGTGGAGCTCTGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC	63
QY	61	TGTGAGAGCTC-GGATTCACCTTTACTAGGAATCCATGAGCTGGGTAGCCAGGCTCCA	119
Db	64	TGTGAGAGCTC-GGATTCACCTTTACTAGGAATCCATGAGCTGGGTAGCCAGGCTCCA	123
QY	120	GGGAAGGGCTGGAGTGGGTGTTTAAATATATGTTAGTGGGAATGGAACCACTATGCG	179
Db	124	GGCAAGGGCTGGAGTGGGTGTTTAAATATATGTTAGTGGGAATGGAACCACTATGCG	183
QY	180	GACTCTGTGAGGGCCGATTCACCATCTCCAGAGCAACGCCAAGCACTCATGTATCTG	239
Db	184	GACTCCGTGAGGGCCGATTCACCATCTCCAGAGCAATCCAGAGCACTCATGTATCTG	243
QY	240	CAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGATCTGT	299
Db	244	CAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG-----	295
QY	300	CTTATGACAGAGGCTACTTTGACTACTGTGGGGCCAGGAACCCCTGGTCCCGTCTCTCA	358

